



SEQUENCE LISTING

<110> BERGER, Dieter et al.

<120> MEANS AND METHODS FOR MODULATING STOMATA CHARACTERISTICA IN PLANTS

<130> 0147-0223P

<140> 09/806,767

<141> 2001-04-03

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<170> PatentIn version 3.1

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His Pro Asn Ser Glu Thr Ala Lys Thr Phe Ala Ser Lys Phe Asp Trp
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Glu Glu Pro Ser Ser Arg Leu Leu Tyr Ser Tyr Gly Ser Ala Ile Glu
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His Thr Ala Ser Thr Val Gly Gly Ser Ser Val Ser Met Ala Asn Val
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His Pro Asn Ser Glu Thr Ala Lys Thr Phe Ala Ser Lys Phe Asp Trp
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His Leu Ser Phe Leu Gln Glu Ala Val Leu Gly Val Glu Glu Glu Glu
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Glu Glu Pro Ser Ser Arg Leu Leu Tyr Ser Tyr Gly Ser Ala Ile Glu
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Gly Phe Ala Ala Gln Leu Thr Glu Ser Glu Ala Glu Ile Leu Arg Tyr
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Ser Pro Glu Val Val Ala Val Arg Pro Asp His Val Leu Gln Val Gln
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Leu Asp Thr Gly Val Trp Pro Glu Ser Pro Ser Phe Asp Asp Thr Gly
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Met Pro Ser Ile Pro Arg Lys Trp Lys Gly Ile Cys Gln Glu Gly Glu
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Ser Phe Ser Ser Ser Ser Cys Asn Arg Lys Leu Ile Gly Ala Arg Phe
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Phe Ile Arg Gly His Arg Val Ala Asn Ser Pro Glu Glu Ser Pro Asn
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Met Pro Arg Glu Tyr Ile Ser Ala Arg Asp Ser Thr Gly His Gly Thr
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His Thr Ala Ser Thr Val Gly Gly Ser Ser Val Ser Met Ala Asn Val
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Leu Gly Asn Gly Ala Gly Val Ala Arg Gly Met Ala Pro Gly Ala His
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aat gag cta aag gca ctg aag aaa tcg aat aat gtg tta tca ata tat Asn Glu Leu Lys Ala Leu Lys Lys Ser Asn Asn Val Leu Ser Ile Tyr 145 150 155	479
ccg gag agg aag ctt gag gtt caa aca act tat tct tac aag ttc tta Pro Glu Arg Lys Leu Glu Val Gln Thr Thr Tyr Ser Tyr Lys Phe Leu 160 165 170 175	527
gga ctt agt cct aca aag gaa ggt act tgg tta aag tct gga ttt ggt Gly Leu Ser Pro Thr Lys Glu Gly Thr Trp Leu Lys Ser Gly Phe Gly 180 185 190	575
cga ggc gcg atc att gga gtt ctt gat act gga att tgg cca gaa agt Arg Gly Ala Ile Ile Gly Val Leu Asp Thr Gly Ile Trp Pro Glu Ser 195 200 205	623
cca agt ttt gtt gat cat gga atg tct cct att cca aag aaa tgg aaa Pro Ser Phe Val Asp His Gly Met Ser Pro Ile Pro Lys Lys Trp Lys 210 215 220	671

ggt ntc tgc caa gaa gga aaa aac ttc aat tct tca agt tgc aat cgc Gly Xaa Cys Gln Glu Gly Lys Asn Phe Asn Ser Ser Ser Cys Asn Arg 225 230 235	719
aag ctt att ggt gca agg ttt ttc cag ata gga cac atg atg gca tca Lys Leu Ile Gly Ala Arg Phe Phe Gln Ile Gly His Met Met Ala Ser 240 245 250 255	767
aag aca tca aaa tca ata gat ttt atg gag gat tat gta tca cct cga Lys Thr Ser Lys Ser Ile Asp Phe Met Glu Asp Tyr Val Ser Pro Arg 260 265 270	815
gat tct caa ggc cat ggt aca cat aca gca tct act gca ggg gga gct Asp Ser Gln Gly His Gly Thr His Thr Ala Ser Thr Ala Gly Gly Ala 275 280 285	863
ccc gtt cca atg gcg agt gtg ctt gga aat gga gca gga gag gct cga Pro Val Pro Met Ala Ser Val Leu Gly Asn Gly Ala Gly Glu Ala Arg 290 295 300	911
ggg atg gcc cct ggt gct cat atc gcg ata tac aaa gtt tgt tgg tct Gly Met Ala Pro Gly Ala His Ile Ala Ile Tyr Lys Val Cys Trp Ser 305 310 315	959
agt ggt tgt tat agt tct gat ata ctt gca gca atg gat gta gct att Ser Gly Cys Tyr Ser Ser Asp Ile Leu Ala Ala Met Asp Val Ala Ile 320 325 330 335	1007
aga gat gga gta gac ata ttg tct ctt tca att ggt ggt ttc cct gtt Arg Asp Gly Val Asp Ile Leu Ser Leu Ser Ile Gly Gly Phe Pro Val 340 345 350	1055
cca ctt tat gag gat act att gct att ggc agt ttt cga gct atg gaa Pro Leu Tyr Glu Asp Thr Ile Ala Ile Gly Ser Phe Arg Ala Met Glu 355 360 365	1103
cgt gga att tca gtt ata tgt gct gca gga aat aat ggt cca att cta Arg Gly Ile Ser Val Ile Cys Ala Ala Gly Asn Asn Gly Pro Ile Leu 370 375 380	1151
agt tca gta gca aat gag gct cct tgg att gcc act att ggt gct agc Ser Ser Val Ala Asn Glu Ala Pro Trp Ile Ala Thr Ile Gly Ala Ser 385 390 395	1199
aca ctt gac agg aaa ttt cca gca ata att cag cta ggt aat ggc aag Thr Leu Asp Arg Lys Phe Pro Ala Ile Ile Gln Leu Gly Asn Gly Lys 400 405 410 415	1247
tat gtg tat gga gaa tcc ttg tac ccg ggc aaa caa gtt cat aat tct Tyr Val Tyr Gly Glu Ser Leu Tyr Pro Gly Lys Gln Val His Asn Ser 420 425 430	1295
cag aaa gtt ctt gag att gtt tat ctc aat gac ggt gat aat gga agt Gln Lys Val Leu Glu Ile Val Tyr Leu Asn Asp Gly Asp Asn Gly Ser 435 440 445	1343

gaa ttt tgc tta aga ggg tct ctg cca aga gct aaa gtc cat gga aaa Glu Phe Cys Leu Arg Gly Ser Leu Pro Arg Ala Lys Val His Gly Lys 450 455 460	1391
atc gtt gta tgt gat cgt gga gtt aat gga aga gca gag aaa ggt caa Ile Val Val Cys Asp Arg Gly Val Asn Gly Arg Ala Glu Lys Gly Gln 465 470 475	1439
gtt gtt aaa gaa tca ggt ggt gtt gcc atg atc cta gca aat aca gca Val Val Lys Glu Ser Gly Gly Val Ala Met Ile Leu Ala Asn Thr Ala 480 485 490 495	1487
gta aat atg gag gaa gat tct gtg gac gta cat gtc cta cct gca aca Val Asn Met Glu Glu Asp Ser Val Asp Val His Val Leu Pro Ala Thr 500 505 510	1535
ttg att ggt ttt gac gaa tca att cag ttg caa agc tat atg aac tca Leu Ile Gly Phe Asp Glu Ser Ile Gln Leu Gln Ser Tyr Met Asn Ser 515 520 525	1583
acg cga aaa cca aca gct cga atc ata ttt gga gga aca gtt ata gga Thr Arg Lys Pro Thr Ala Arg Ile Ile Phe Gly Gly Thr Val Ile Gly 530 535 540	1631
aaa tct agt gca cct gct gta gca caa ttt tct tca agg ggt cca agt Lys Ser Ser Ala Pro Ala Val Ala Gln Phe Ser Ser Arg Gly Pro Ser 545 550 555	1679
ttt act gat cct tca att ctc aaa cct gat gtg att gct cca ggt gtc Phe Thr Asp Pro Ser Ile Leu Lys Pro Asp Val Ile Ala Pro Gly Val 560 565 570 575	1727
aac ata att gct gct tgg ccg caa aat cta ggt cct agt ggc ctg gct Asn Ile Ile Ala Ala Trp Pro Gln Asn Leu Gly Pro Ser Gly Leu Ala 580 585 590	1775
gag gat tca aga aga gta aac ttc act gtc tta tca gga act tca atg Glu Asp Ser Arg Arg Val Asn Phe Thr Val Leu Ser Gly Thr Ser Met 595 600 605	1823
gct tgt cct cat gtt agt ggc att gct gca cta ctc cat tca att cat Ala Cys Pro His Val Ser Gly Ile Ala Ala Leu Leu His Ser Ile His 610 615 620	1871
cct aaa tgg tca cca gct gca atc aaa tcc gcg cta atg aca act gca Pro Lys Trp Ser Pro Ala Ala Ile Lys Ser Ala Leu Met Thr Thr Ala 625 630 635	1919
gac aca aca aac cac caa gga aaa cca atc atg gat ggt gac aca cga Asp Thr Thr Asn His Gln Gly Lys Pro Ile Met Asp Gly Asp Thr Arg 640 645 650 655	1967
gct gga ctt ttc gcc ata gga gct gga cat gta aat cct gga aga tcc Ala Gly Leu Phe Ala Ile Gly Ala Gly His Val Asn Pro Gly Arg Ser 660 665 670	2015

gat gat ccc gga ttg ata tat gac att aat gca aat gac tat atc act Asp Asp Pro Gly Leu Ile Tyr Asp Ile Asn Ala Asn Asp Tyr Ile Thr 675 680 685	2063
cac ctt tgc act att ggt tac aaa aac tct gaa atc ctc agc att act His Leu Cys Thr Ile Gly Tyr Lys Asn Ser Glu Ile Leu Ser Ile Thr 690 695 700	2111
cac aag aat gtt agc tgc cac gac gtt tta cag aaa aac agg ggt ttt His Lys Asn Val Ser Cys His Asp Val Leu Gln Lys Asn Arg Gly Phe 705 710 715	2159
agt ctc aat tac ccc tct att tcc gta atc ttt aag gca gga aaa acg Ser Leu Asn Tyr Pro Ser Ile Ser Val Ile Phe Lys Ala Gly Lys Thr 720 725 730 735	2207
aga aaa atg atc aca agg aga gtg aca aat gtg ggg agt cct aat tca Arg Lys Met Ile Thr Arg Arg Val Thr Asn Val Gly Ser Pro Asn Ser 740 745 750	2255
atc tac tca gtt gaa att gtg gca cca gaa gga gtt aaa gtg aga gtt Ile Tyr Ser Val Glu Ile Val Ala Pro Glu Gly Val Lys Val Arg Val 755 760 765	2303
aaa ccg cga cgt ctg gta ttt aaa cat gtt aat caa agt tta agt tac Lys Pro Arg Arg Leu Val Phe Lys His Val Asn Gln Ser Leu Ser Tyr 770 775 780	2351
aga gtt tgg ttt ata tca agg aag aga att ggg act caa agg aga agc Arg Val Trp Phe Ile Ser Arg Lys Arg Ile Gly Thr Gln Arg Arg Ser 785 790 795	2399
ttt gca gaa gga caa ttg atg tgg atc aac tcc aga gat aaa tac cag Phe Ala Glu Gly Gln Leu Met Trp Ile Asn Ser Arg Asp Lys Tyr Gln 800 805 810 815	2447
aaa gtt aga agt cct att tca gtt gca tgg gca tca aag aag tga Lys Val Arg Ser Pro Ile Ser Val Ala Trp Ala Ser Lys Lys 820 825	2492

<210> 10
 <211> 829
 <212> PRT
 <213> Solanum tuberosum

 <220>
 <221> misc_feature
 <222> (225)..(225)
 <223> The 'Xaa' at location 225 stands for Ile, Val, Leu, or Phe.

 <400> 10

Ile	Leu	Phe	Asn	Pro	Phe	Lys	Tyr	Pro	His	Gln	Ile	Ile	Ser	Thr	Asn
1				5					10						15

Ile Pro Leu Phe Asn Phe Lys Tyr Asn Ser Met Glu Leu Asn Phe Gln
 20 25 30

Phe Tyr Phe Leu Cys Phe Leu Leu Cys Phe Ile Pro Leu Leu Gln Ala
 35 40 45

Gln Asn Leu Gln Thr Tyr Ile Val Gln Leu His Pro Gln His Ala Ser
 50 55 60

Thr Arg Thr Pro Phe Ser Ser Lys Phe Gln Trp His Leu Ser Phe Leu
 65 70 75 80

Glu Asn Phe Thr Asn Ile Pro Leu Phe Asn Phe Lys Tyr Ile Gln Trp
 85 90 95

Asn Ser Ile Pro Ile Leu Phe Leu Cys Phe Tyr Ser Val Tyr Ser Pro
 100 105 110

Ala Thr Ser Ile Ser Ser Gly Glu Asn Ser Ser Ser Arg Leu Leu Tyr
 115 120 125

Ser Tyr His Ser Ala Phe Glu Gly Phe Ala Ala Leu Leu Ser Glu Asn
 130 135 140

Glu Leu Lys Ala Leu Lys Lys Ser Asn Asn Val Leu Ser Ile Tyr Pro
 145 150 155 160

Glu Arg Lys Leu Glu Val Gln Thr Thr Tyr Ser Tyr Lys Phe Leu Gly
 165 170 175

Leu Ser Pro Thr Lys Glu Gly Thr Trp Leu Lys Ser Gly Phe Gly Arg
 180 185 190

Gly Ala Ile Ile Gly Val Leu Asp Thr Gly Ile Trp Pro Glu Ser Pro
 195 200 205

Ser Phe Val Asp His Gly Met Ser Pro Ile Pro Lys Lys Trp Lys Gly
 210 215 220

Xaa Cys Gln Glu Gly Lys Asn Phe Asn Ser Ser Ser Cys Asn Arg Lys
 225 230 235 240

Leu Ile Gly Ala Arg Phe Phe Gln Ile Gly His Met Met Ala Ser Lys
 245 250 255

Thr Ser Lys Ser Ile Asp Phe Met Glu Asp Tyr Val Ser Pro Arg Asp
 260 265 270

Ser Gln Gly His Gly Thr His Thr Ala Ser Thr Ala Gly Gly Ala Pro
 275 280 285

Val Pro Met Ala Ser Val Leu Gly Asn Gly Ala Gly Glu Ala Arg Gly
 290 295 300

Met Ala Pro Gly Ala His Ile Ala Ile Tyr Lys Val Cys Trp Ser Ser
 305 310 315 320

Gly Cys Tyr Ser Ser Asp Ile Leu Ala Ala Met Asp Val Ala Ile Arg
 325 330 335

Asp Gly Val Asp Ile Leu Ser Leu Ser Ile Gly Gly Phe Pro Val Pro
 340 345 350

Leu Tyr Glu Asp Thr Ile Ala Ile Gly Ser Phe Arg Ala Met Glu Arg
 355 360 365

Gly Ile Ser Val Ile Cys Ala Ala Gly Asn Asn Gly Pro Ile Leu Ser
 370 375 380

Ser Val Ala Asn Glu Ala Pro Trp Ile Ala Thr Ile Gly Ala Ser Thr
 385 390 395 400

Leu Asp Arg Lys Phe Pro Ala Ile Ile Gln Leu Gly Asn Gly Lys Tyr
 405 410 415

Val Tyr Gly Glu Ser Leu Tyr Pro Gly Lys Gln Val His Asn Ser Gln
 420 425 430

Lys Val Leu Glu Ile Val Tyr Leu Asn Asp Gly Asp Asn Gly Ser Glu
 435 440 445

Phe Cys Leu Arg Gly Ser Leu Pro Arg Ala Lys Val His Gly Lys Ile
 450 455 460

Val Val Cys Asp Arg Gly Val Asn Gly Arg Ala Glu Lys Gly Gln Val
 465 470 475 480

Val Lys Glu Ser Gly Gly Val Ala Met Ile Leu Ala Asn Thr Ala Val
 485 490 495

Asn Met Glu Glu Asp Ser Val Asp Val His Val Leu Pro Ala Thr Leu
 500 505 510

Ile Gly Phe Asp Glu Ser Ile Gln Leu Gln Ser Tyr Met Asn Ser Thr
 515 520 525

Arg Lys Pro Thr Ala Arg Ile Ile Phe Gly Gly Thr Val Ile Gly Lys
 530 535 540

Ser Ser Ala Pro Ala Val Ala Gln Phe Ser Ser Arg Gly Pro Ser Phe
 545 550 555 560

Thr Asp Pro Ser Ile Leu Lys Pro Asp Val Ile Ala Pro Gly Val Asn
 565 570 575

Ile Ile Ala Ala Trp Pro Gln Asn Leu Gly Pro Ser Gly Leu Ala Glu
 580 585 590

Asp Ser Arg Arg Val Asn Phe Thr Val Leu Ser Gly Thr Ser Met Ala
 595 600 605

Cys Pro His Val Ser Gly Ile Ala Ala Leu Leu His Ser Ile His Pro
 610 615 620

Lys Trp Ser Pro Ala Ala Ile Lys Ser Ala Leu Met Thr Thr Ala Asp
 625 630 635 640

Thr Thr Asn His Gln Gly Lys Pro Ile Met Asp Gly Asp Thr Arg Ala
 645 650 655

Gly Leu Phe Ala Ile Gly Ala Gly His Val Asn Pro Gly Arg Ser Asp
 660 665 670

Asp Pro Gly Leu Ile Tyr Asp Ile Asn Ala Asn Asp Tyr Ile Thr His
 675 680 685

Leu Cys Thr Ile Gly Tyr Lys Asn Ser Glu Ile Leu Ser Ile Thr His
690 695 700

Lys Asn Val Ser Cys His Asp Val Leu Gln Lys Asn Arg Gly Phe Ser
705 710 715 720

Leu Asn Tyr Pro Ser Ile Ser Val Ile Phe Lys Ala Gly Lys Thr Arg
725 730 735

Lys Met Ile Thr Arg Arg Val Thr Asn Val Gly Ser Pro Asn Ser Ile
740 745 750

Tyr Ser Val Glu Ile Val Ala Pro Glu Gly Val Lys Val Arg Val Lys
755 760 765

Pro Arg Arg Leu Val Phe Lys His Val Asn Gln Ser Leu Ser Tyr Arg
770 775 780

Val Trp Phe Ile Ser Arg Lys Arg Ile Gly Thr Gln Arg Arg Ser Phe
785 790 795 800

Ala Glu Gly Gln Leu Met Trp Ile Asn Ser Arg Asp Lys Tyr Gln Lys
805 810 815

Val Arg Ser Pro Ile Ser Val Ala Trp Ala Ser Lys Lys
820 825

<210> 11
<211> 3140
<212> DNA
<213> Solanum tuberosum

<220>
<221> CDS
<222> (1)..(2298)
<223>

<220>
<221> misc_feature
<222> (2549)..(2549)
<223> n is any nucleotide base (a, t, g, or c)

<400> 11

act cat tta ttc tcc ttt cta tgt ctt tta cta tgt ttt gtt tgc ata Thr His Leu Phe Ser Phe Leu Cys Leu Leu Leu Cys Phe Val Cys Ile 1 5 10 15	48
caa gct caa gat ttg caa act tac ata gtt cag tta cat cca cat gga Gln Ala Gln Asp Leu Gln Thr Tyr Ile Val Gln Leu His Pro His Gly 20 25 30	96
gca aca aga ccc cct ttt agc tct aaa cta caa tgg cac ctt tct ttc Ala Thr Arg Pro Pro Phe Ser Ser Lys Leu Gln Trp His Leu Ser Phe 35 40 45	144
ctt gca aaa gca gtt tcc tct gga gaa caa gac tcg tct tct cgt ctt Leu Ala Lys Ala Val Ser Ser Gly Glu Gln Asp Ser Ser Ser Arg Leu 50 55 60	192
ttg tac tct tac cat tct gcg atg gaa ggt ttt gca gct cga ctc act Leu Tyr Ser Tyr His Ser Ala Met Glu Gly Phe Ala Ala Arg Leu Thr 65 70 75 80	240
gaa gat gag gtt gag ttg tta agg gaa tct aat gat gtg ttg tcg ata Glu Asp Glu Val Glu Leu Leu Arg Glu Ser Asn Asp Val Leu Ser Ile 85 90 95	288
cgt gct gag agg agg ctt gaa att cag act act tat tct tac aag ttc Arg Ala Glu Arg Arg Leu Glu Ile Gln Thr Thr Tyr Ser Tyr Lys Phe 100 105 110	336
ttg gga tta agt cca acg aga gaa gga gct tgg ttg aag tct gga ttt Leu Gly Leu Ser Pro Thr Arg Glu Gly Ala Trp Leu Lys Ser Gly Phe 115 120 125	384
ggt cga ggg gcg atc att gga gtg ttg gat act gga gtt tgg cca gaa Gly Arg Gly Ala Ile Ile gga Val Leu Asp Thr Gly Val Trp Pro Glu 130 135 140	432
agt cca agt ttt gat gat cat ggg atg cca cct gct cca cag aag tgg Ser Pro Ser Phe Asp Asp His Gly Met Pro Pro Ala Pro Gln Lys Trp 145 150 155 160	480
agg ggt gtc tgc caa gga gga cag gat ttt aat tct tct agt tgt aat Arg Gly Val Cys Gln Gly Gly Gln Asp Phe Asn Ser Ser Ser Cys Asn 165 170 175	528
cgc aag ctt att ggt gca agg ttt ttc aga aaa gga cat cgt gtg gct Arg Lys Leu Ile Gly Ala Arg Phe Phe Arg Lys Gly His Arg Val Ala 180 185 190	576
tca atg aca tca tca cca gat gca gtg gag gaa tat gtg tcg cca cgg Ser Met Thr Ser Ser Pro Asp Ala Val Glu Glu Tyr Val Ser Pro Arg 195 200 205	624
gat tcc cat ggc cat ggt aca cat aca gca tcc act gct gga gga gct Asp Ser His Gly His Gly Thr His Thr Ala Ser Thr Ala Gly Gly Ala 210 215 220	672

gca gtt cca ttg gct ggt gtg ctc gga aat gga gca ggg gag gct cga Ala Val Pro Leu Ala Gly Val Leu Gly Asn Gly Ala Gly Glu Ala Arg 225 230 235 240	720
ggg atg gcc ccg ggt gcc cac att gca ata tat aaa gta tgc tgg ttc Gly Met Ala Pro Gly Ala His Ile Ala Ile Tyr Lys Val Cys Trp Phe 245 250 255	768
agt ggt tgt tac agc tct gat ata ctt gca gca atg gat gtg gcc atc Ser Gly Cys Tyr Ser Ser Asp Ile Leu Ala Ala Met Asp Val Ala Ile 260 265 270	816
aga gat gga gta gac ata ttg tca ctc tca ctt ggt ggc ttc cct att Arg Asp Gly Val Asp Ile Leu Ser Leu Ser Leu Gly Gly Phe Pro Ile 275 280 285	864
cca ctt tat gat gat act att gcc att gga agt ttc cga gcc atg gag Pro Leu Tyr Asp Asp Thr Ile Ala Ile Gly Ser Phe Arg Ala Met Glu 290 295 300	912
cat gga att tca gtt ata tgt gct gca ggg aat aat gga cca atc caa His Gly Ile Ser Val Ile Cys Ala Ala Gly Asn Asn Gly Pro Ile Gln 305 310 315 320	960
agt tca gta gcc aac ggt gct cct tgg att gcc act att ggt gct agc Ser Ser Val Ala Asn Gly Ala Pro Trp Ile Ala Thr Ile Gly Ala Ser 325 330 335	1008
aca ctt gac agg aga ttt cca gcg tca gtt cag tta ggc aac gga aag Thr Leu Asp Arg Arg Phe Pro Ala Ser Val Gln Leu Gly Asn Gly Lys 340 345 350	1056
ttc ctg tac gga gaa tcc ttg tac cct ggg aag aaa gtt cct agc tct Phe Leu Tyr Gly Glu Ser Leu Tyr Pro Gly Lys Lys Val Pro Ser Ser 355 360 365	1104
cag aag aat ctt gag atc gtt tat gta aag gat aag gac aag gga agt Gln Lys Asn Leu Glu Ile Val Tyr Val Lys Asp Lys Asp Lys Gly Ser 370 375 380	1152
gaa ttt tgc ttg aga gga tcg cta tca aaa gca caa gtc cga ggg aaa Glu Phe Cys Leu Arg Gly Ser Leu Ser Lys Ala Gln Val Arg Gly Lys 385 390 395 400	1200
atg gtt gtg tgt gat agg gga gtc aat gga agg gca gaa aaa ggc cag Met Val Val Cys Asp Arg Gly Val Asn Gly Arg Ala Glu Lys Gly Gln 405 410 415	1248
gtt gtg aag gag gca ggt ggt gct gcc atg atc tta gca aat aca gca Val Val Lys Glu Ala Gly Gly Ala Ala Met Ile Leu Ala Asn Thr Ala 420 425 430	1296
ata aat atg gag gaa gat tcc att gat gtc cat gtc ctc cca gca acg Ile Asn Met Glu Glu Asp Ser Ile Asp Val His Val Leu Pro Ala Thr 435 440 445	1344

ttg att ggc ttc gat gaa tca att caa tta caa aac tac ctg aac tca Leu Ile Gly Phe Asp Glu Ser Ile Gln Leu Gln Asn Tyr Leu Asn Ser 450 455 460	1392
aca aaa aga cca aca gct cga ttc ata ttt gga gga acg gta ata gga Thr Lys Arg Pro Thr Ala Arg Phe Ile Phe Gly Gly Thr Val Ile Gly 465 470 475 480	1440
aag tct aga gca cct gca gta gct cag ttt tcg tca agg ggg cca agc Lys Ser Arg Ala Pro Ala Val Ala Gln Phe Ser Ser Arg Gly Pro Ser 485 490 495	1488
tat act gat cct tca att ctc aaa cct gat ttg att gct cca ggg gta Tyr Thr Asp Pro Ser Ile Leu Lys Pro Asp Leu Ile Ala Pro Gly Val 500 505 510	1536
aac ata att gcc gct tgg cca caa aac tta ggc ccc agt ggt ctt ccc Asn Ile Ile Ala Ala Trp Pro Gln Asn Leu Gly Pro Ser Gly Leu Pro 515 520 525	1584
gaa gat tca cga aga gta aat ttc act gtt atg tca ggg acc tca atg Glu Asp Ser Arg Arg Val Asn Phe Thr Val Met Ser Gly Thr Ser Met 530 535 540	1632
gca tgt cct cat gta agt gga att gcc gca ttg ctc cat tca gct cat Ala Cys Pro His Val Ser Gly Ile Ala Ala Leu Leu His Ser Ala His 545 550 555 560	1680
cct aaa tgg act cca gca gca ata aga tcc gca tta atg acc act gca Pro Lys Trp Thr Pro Ala Ala Ile Arg Ser Ala Leu Met Thr Thr Ala 565 570 575	1728
gat aca gct gat cat atg gga aaa cca atc atg gat gga gat gca cca Asp Thr Ala Asp His Met Gly Lys Pro Ile Met Asp Gly Asp Ala Pro 580 585 590	1776
gct aaa ctt ttt gca gct gga gct gga cac gtg aac cct gga aga gcc Ala Lys Leu Phe Ala Ala Gly Ala Gly His Val Asn Pro Gly Arg Ala 595 600 605	1824
atc gat cct gga ttg ata tat gac atc cag gtt gat gaa tat atc act Ile Asp Pro Gly Leu Ile Tyr Asp Ile Gln Val Asp Glu Tyr Ile Thr 610 615 620	1872
cat ctt tgc act atc gga tac aga aat tct gaa gtc ttc agc att act His Leu Cys Thr Ile Gly Tyr Arg Asn Ser Glu Val Phe Ser Ile Thr 625 630 635 640	1920
cat agg aat gtc agc tgc cat gac att tta cag aac aac agg ggt ttc His Arg Asn Val Ser Cys His Asp Ile Leu Gln Asn Asn Arg Gly Phe 645 650 655	1968
agc cta aat tac ccc tca att tca ata act ttc aga gca gga atg act Ser Leu Asn Tyr Pro Ser Ile Ser Ile Thr Phe Arg Ala Gly Met Thr 660 665 670	2016

aga aag ata-atc aag agg aga gta aca aat gtg ggg aac cct aac tct Arg Lys Ile Ile Lys Arg Arg Val Thr Asn Val Gly Asn Pro Asn Ser 675 680 685	2064
att tac tca gtt gac att gag gca cct gag gga gtc aaa gtg aga gtg Ile Tyr Ser Val Asp Ile Glu Ala Pro Glu Gly Val Lys Val Arg Val 690 695 700	2112
aag cca cgt cgt ctg ata ttt aaa cat gtg aac caa agc tta agc tat Lys Pro Arg Arg Leu Ile Phe Lys His Val Asn Gln Ser Leu Ser Tyr 705 710 715 720	2160
aga gtt tgg ttt ata tca cga aag awa ata gag tct aaa agg atg agc Arg Val Trp Phe Ile Ser Arg Lys Xaa Ile Glu Ser Lys Arg Met Ser 725 730 735	2208
ttt gca gag ggg caa ttg aca tgg ttc aat gta gga aac aaa gcc acg Phe Ala Glu Gly Gln Leu Thr Trp Phe Asn Val Gly Asn Lys Ala Thr 740 745 750	2256
aaa gtt aaa agt cct att tcc gtc aca tgg gca tca atg aag Lys Val Lys Ser Pro Ile Ser Val Thr Trp Ala Ser Met Lys 755 760 765	2298
tgatcactat caccactatc acaagcacca tatatttcat tgtcttagtt caaaatttcc	2358
aattaggaat ttcacatcac attataaatt gatgttagag cagatacact ttatctttcc	2418
acaaagaaga aatgatcgat aatcattgaa atgatttgtg ttttactaag tagatgtgtc	2478
tccacaatgt taagaagtat taatatgtat aaatagatta gacaaagcac gagattgcgc	2538
ctgagtgagg nattttctca agtttacacc ttttgaacta aattactcat aaaccagtat	2598
gacagacaaa aaattcaaga aattggcgag gcaaaagaaa acatacaata taatctcaac	2658
ttttaacaaa ttgcaagcca tttgaattag cataccgctc cataaatctc atgaacctgt	2718
cccagtctcg tggagtccgc ataataact tagcttcaat tcctgcaggc tttccattaa	2778
caaacttagc attgacatca actgacgtta gaaccccttc ttcgtcaatc atgtagaatc	2838
cagtgatatc ccctacttca ccagatgaat caaatacgga gggttgatca aacctgaata	2898
tagccatacc atttgtccat cccttgactt tgtaatttc acatctggtg ttgtttgctc	2958
atcagttcct tgtatgaact gaatTTTTGG ttgaaccatc attatacata gtctggacat	3018
tttctggttt ttgatattgg tactgaaacg cgaacgggat aggcacaatc gttggccaat	3078
tgaatgaaga acctgcactt tgatgaacta tccttgatgc tattcctaca gtacatgaca	3138
ca	3140

<210> 12

<211> 766
 <212> PRT
 <213> Solanum tuberosum

<220>
 <221> misc_feature
 <222> (729)..(729)
 <223> The 'Xaa' at location 729 stands for Lys, or Ile.

<400> 12

Thr His Leu Phe Ser Phe Leu Cys Leu Leu Leu Cys Phe Val Cys Ile
 1 5 10 15

Gln Ala Gln Asp Leu Gln Thr Tyr Ile Val Gln Leu His Pro His Gly
 20 25 30

Ala Thr Arg Pro Pro Phe Ser Ser Lys Leu Gln Trp His Leu Ser Phe
 35 40 45

Leu Ala Lys Ala Val Ser Ser Gly Glu Gln Asp Ser Ser Ser Arg Leu
 50 55 60

Leu Tyr Ser Tyr His Ser Ala Met Glu Gly Phe Ala Ala Arg Leu Thr
 65 70 75 80

Glu Asp Glu Val Glu Leu Leu Arg Glu Ser Asn Asp Val Leu Ser Ile
 85 90 95

Arg Ala Glu Arg Arg Leu Glu Ile Gln Thr Thr Tyr Ser Tyr Lys Phe
 100 105 110

Leu Gly Leu Ser Pro Thr Arg Glu Gly Ala Trp Leu Lys Ser Gly Phe
 115 120 125

Gly Arg Gly Ala Ile Ile Gly Val Leu Asp Thr Gly Val Trp Pro Glu
 130 135 140

Ser Pro Ser Phe Asp Asp His Gly Met Pro Pro Ala Pro Gln Lys Trp
 145 150 155 160

Arg Gly Val Cys Gln Gly Gly Gln Asp Phe Asn Ser Ser Ser Cys Asn
 165 170 175

Arg Lys Leu Ile Gly Ala Arg Phe Phe Arg Lys Gly His Arg Val Ala
 180 185 190

Ser Met Thr Ser Ser Pro Asp Ala Val Glu Glu Tyr Val Ser Pro Arg
 195 200 205

Asp Ser His Gly His Gly Thr His Thr Ala Ser Thr Ala Gly Gly Ala
 210 215 220

Ala Val Pro Leu Ala Gly Val Leu Gly Asn Gly Ala Gly Glu Ala Arg
 225 230 235 240

Gly Met Ala Pro Gly Ala His Ile Ala Ile Tyr Lys Val Cys Trp Phe
 245 250 255

Ser Gly Cys Tyr Ser Ser Asp Ile Leu Ala Ala Met Asp Val Ala Ile
 260 265 270

Arg Asp Gly Val Asp Ile Leu Ser Leu Ser Leu Gly Gly Phe Pro Ile
 275 280 285

Pro Leu Tyr Asp Asp Thr Ile Ala Ile Gly Ser Phe Arg Ala Met Glu
 290 295 300

His Gly Ile Ser Val Ile Cys Ala Ala Gly Asn Asn Gly Pro Ile Gln
 305 310 315 320

Ser Ser Val Ala Asn Gly Ala Pro Trp Ile Ala Thr Ile Gly Ala Ser
 325 330 335

Thr Leu Asp Arg Arg Phe Pro Ala Ser Val Gln Leu Gly Asn Gly Lys
 340 345 350

Phe Leu Tyr Gly Glu Ser Leu Tyr Pro Gly Lys Lys Val Pro Ser Ser
 355 360 365

Gln Lys Asn Leu Glu Ile Val Tyr Val Lys Asp Lys Asp Lys Gly Ser
 370 375 380

Glu Phe Cys Leu Arg Gly Ser Leu Ser Lys Ala Gln Val Arg Gly Lys
 385 390 395 400

Met Val Val Cys Asp Arg Gly Val Asn Gly Arg Ala Glu Lys Gly Gln
 405 410 415

Val Val Lys Glu Ala Gly Gly Ala Ala Met Ile Leu Ala Asn Thr Ala
 420 425 430

Ile Asn Met Glu Glu Asp Ser Ile Asp Val His Val Leu Pro Ala Thr
 435 440 445

Leu Ile Gly Phe Asp Glu Ser Ile Gln Leu Gln Asn Tyr Leu Asn Ser
 450 455 460

Thr Lys Arg Pro Thr Ala Arg Phe Ile Phe Gly Gly Thr Val Ile Gly
 465 470 475 480

Lys Ser Arg Ala Pro Ala Val Ala Gln Phe Ser Ser Arg Gly Pro Ser
 485 490 495

Tyr Thr Asp Pro Ser Ile Leu Lys Pro Asp Leu Ile Ala Pro Gly Val
 500 505 510

Asn Ile Ile Ala Ala Trp Pro Gln Asn Leu Gly Pro Ser Gly Leu Pro
 515 520 525

Glu Asp Ser Arg Arg Val Asn Phe Thr Val Met Ser Gly Thr Ser Met
 530 535 540

Ala Cys Pro His Val Ser Gly Ile Ala Ala Leu Leu His Ser Ala His
 545 550 555 560

Pro Lys Trp Thr Pro Ala Ala Ile Arg Ser Ala Leu Met Thr Thr Ala
 565 570 575

Asp Thr Ala Asp His Met Gly Lys Pro Ile Met Asp Gly Asp Ala Pro
 580 585 590

Ala Lys Leu Phe Ala Ala Gly Ala Gly His Val Asn Pro Gly Arg Ala
 595 600 605

Ile Asp Pro Gly Leu Ile Tyr Asp Ile Gln Val Asp Glu Tyr Ile Thr
 610 615 620

His Leu Cys Thr Ile Gly Tyr Arg Asn Ser Glu Val Phe Ser Ile Thr
 625 630 635 640

His Arg Asn Val Ser Cys His Asp Ile Leu Gln Asn Asn Arg Gly Phe
 645 650 655

Ser Leu Asn Tyr Pro Ser Ile Ser Ile Thr Phe Arg Ala Gly Met Thr
 660 665 670

Arg Lys Ile Ile Lys Arg Arg Val Thr Asn Val Gly Asn Pro Asn Ser
 675 680 685

Ile Tyr Ser Val Asp Ile Glu Ala Pro Glu Gly Val Lys Val Arg Val
 690 695 700

Lys Pro Arg Arg Leu Ile Phe Lys His Val Asn Gln Ser Leu Ser Tyr
 705 710 715 720

Arg Val Trp Phe Ile Ser Arg Lys Xaa Ile Glu Ser Lys Arg Met Ser
 725 730 735

Phe Ala Glu Gly Gln Leu Thr Trp Phe Asn Val Gly Asn Lys Ala Thr
 740 745 750

Lys Val Lys Ser Pro Ile Ser Val Thr Trp Ala Ser Met Lys
 755 760 765

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<220>
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<400> 13

Gln Thr Tyr Ile Val
 1 5

<210> 14
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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 14

Ile Val Gln Leu His
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<210> 15

<211> 5

<212> PRT

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<223> Characteristic motif of subtilisin-like serine protease

<400> 15

Ser Ser Arg Leu Leu
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<210> 16

<211> 5

<212> PRT

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<400> 16

Gln Thr Thr Tyr Ser
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<210> 17

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<400> 17

Ser Ser Ser Cys Asn
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<210> 18

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 18

Val Leu Gly Asn Gly
1 5

<210> 19

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<212> PRT

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 19

Gly Ala His Ile Ala
1 5

<210> 20

<211> 5

<212> PRT

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 20

Phe Arg Ala Met Glu
1 5

<210> 21

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 21

Val Ile Cys Ala Ala
1 5

<210> 22

<211> 5

<212> PRT

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<400> 22

Ala Ala Gly Asn Asn
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<210> 23

<211> 5

<212> PRT

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<223> Characteristic motif of subtilisin-like serine protease

<400> 23

Ser Ser Val Ala Asn
1 5

<210> 24

<211> 5

<212> PRT

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 24

Tyr Gly Glu Ser Leu
1 5

<210> 25

<211> 5

<212> PRT

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 25

Gly Ser Glu Phe Cys
1 5

<210> 26

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 26

Cys Leu Arg Gly Ser
1 5

<210> 27

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 27

Arg Gly Val Asn Gly
1 5

<210> 28

<211> 6

<212> PRT

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 28

Pro Ala Thr Leu Ile Gly
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<210> 29

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 29

Ile Phe Gly Gly Thr
1 5

<210> 30

<211> 5

<212> PRT

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 30

Pro Gln Asn Leu Gly
1 5

<210> 31

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 31

Val Asn Phe Thr Val
1 5

<210> 32

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 32

His Val Ser Gly Ile
1 5

<210> 33

<211> 5

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<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 33

Gly Phe Ser Leu Asn
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<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 34

Arg Arg Val Thr Asn
1 5

<210> 35

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 35

Pro Asn Ser Ile Tyr
1 5

<210> 36

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 36

Leu Ser Tyr Arg Val
1 5

<210> 37

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Characteristic motif of subtilisin-like serine protease

<400> 37

Ser Pro Ile Ser Val
1 5

<210> 38

<211> 5

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<213> Artificial Sequence

<220>

<223> substrate binding site motif
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 Val Ile Cys Ala Ala
 1 5

 <210> 39
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 Cys Ala Ala Gly Asn
 1 5

 <210> 40
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 <400> 40
 Ala Ala Gly Asn Asn
 1 5

 <210> 41
 <211> 9
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 Val Ile Cys Ala Ala Gly Asn Asn Gly
 1 5

 <210> 42
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<223> D region characteristic motif

<400> 42

Ile Ile Gly Val Leu
1 5

<210> 43 .

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> D region characteristic motif

<400> 43

Gly Val Leu Asp Thr
1 5

<210> 44

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> H region characteristic motif

<400> 44

Thr His Thr Ala Ser Thr
1 5

<210> 45

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> H region characteristic motif .

<400> 45

Ser Arg Asp Ser
1

<210> 46

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> D region characteristic motif

<400> 46

Arg Asp Ser Gly
1

<210> 47

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> S region characteristic motif

<400> 47

His Val Ser Gly Ile
1 5

<210> 48

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> S region characteristic motif

<400> 48

Phe Thr Val Ser Gly Thr
1 5

<210> 49

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 49

Ser Tyr His Ser Ala
1 5

<210> 50

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 50

Gly Leu Ser Pro Thr
1 5

<210> 51

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 51

Trp Leu Lys Ser Gly
1 5

<210> 52

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 52

Phe Asn Ser Ser Ser
1 5

<210> 53

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 53

Ala Ser Thr Ala Gly
1 5

<210> 54

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 54

Ala Ala Met Asp Val
1 5

<210> 55

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 55

Trp Ile Ala Thr Ile
1 5

<210> 56

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 56

Gly Pro Ser Gly Leu
1 5

<210> 57

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 57

Ile Ala Ala Leu Leu His
1 5

<210> 58

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 58

Lys Pro Ile Met Asp
1 5

<210> 59

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 59

Val Ser Cys His Asp
1 5

<210> 60

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 60

Tyr Pro Ser Ile Ser
1 5

<210> 61

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence motif found in subtilisins

<400> 61

Ser Leu Ser Tyr Arg
1 5

<210> 62

<211> 25

<212> PRT

<213> Alnus glutinosa

<400> 62

Gly Glu Asp Val Ile Ile Gly Val Ile Asp Ser Gly Val Trp Pro Glu
1 5 10 15

Ser Asp Ser Phe Lys Asp Asp Gly Met
20 25

<210> 63
<211> 25
<212> PRT
<213> Arabidopsis thaliana

<400> 63

Gly Gln Gly Thr Ile Ile Gly Val Leu Asp Thr Gly Val Trp Pro Glu
1 5 10 15

Ser Pro Ser Phe Asp Asp Thr Gly Met
20 25

<210> 64
<211> 25
<212> PRT
<213> Lycopersicon esculentum

<400> 64

Gly Lys Gly Val Ile Ile Gly Val Ile Asp Thr Gly Ile Leu Pro Asp
1 5 10 15

His Pro Ser Phe Ser Asp Val Gly Met
20 25

<210> 65
<211> 25
<212> PRT
<213> Cucumis melo

<400> 65

Glu Ser Asn Ile Val Val Gly Val Leu Asp Thr Gly Ile Trp Pro Glu
1 5 10 15

Ser Pro Ser Phe Asp Asp Glu Gly Phe
20 25

<210> 66
<211> 25

<212> PRT
<213> Homo sapiens

<400> 66

Gly His Gly Ile Val Val Ser Ile Leu Asp Asp Gly Ile Glu Lys Asn
1 5 10 15

His Pro Asp Leu Ala Gly Asn Tyr Asp
20 25

<210> 67
<211> 25
<212> PRT
<213> Homo sapiens

<400> 67

Gly Lys Gly Val Val Ile Thr Val Leu Asp Asp Gly Leu Glu Trp Asn
1 5 10 15

His Thr Asp Ile Tyr Ala Asn Tyr Asp
20 25

<210> 68
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence found in various yeast species

<400> 68

Gly Ala Gly Val Val Ala Ala Ile Val Asp Asp Gly Leu Asp Tyr Glu
1 5 10 15

Asn Glu Asp Leu Lys Asp Asn Phe Cys
20 25

<210> 69
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence found in various bacteria species

<400> 69

Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser
 1 5 10 15

His Pro Asp Leu Lys Val Ala Gly Gly
 20 25

<210> 70
 <211> 25
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 <213> Artificial Sequence

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<220>
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 <222> (1)..(25)
 <223> Xaa can be any amino acid

<400> 70

Gly Xaa Gly Val Xaa Xaa Val Xaa Asp Xaa Gly Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Pro Xaa Xaa Xaa Asp Xaa Gly Xaa Xaa
 20 25

<210> 71
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 71

Tyr Thr Gln Met Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu
 1 5 10 15

Val Ala Ala Val Ala Asn Asn Gly Val Cys
 20 25

<210> 72
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 72

Tyr Asp Pro Thr Asn Glu Asn Lys His Gly Thr Arg Cys Ala Gly Glu
 1 5 10 15

Ile Ala Met Gln Ala Asn Asn His Lys Cys
20 25

<210> 73
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence found in a various yeast species

<400> 73

Lys Pro Arg Leu Ser Asp Asp Tyr His Gly Thr Arg Cys Ala Gly Glu
1 5 10 15

Ile Ala Ala Lys Lys Gly Asn Asn Phe Cys
20 25

<210> 74
<211> 26
<212> PRT
<213> Cucumis melo

<400> 74

Asn Gly Pro Arg Asp Thr Asn Gly His Gly Thr His Thr Ala Ser Thr
1 5 10 15

Ala Ala Gly Gly Leu Val Ser Gln Ala Asn
20 25

<210> 75
<211> 26
<212> PRT
<213> Lycopersicon esculentum

<400> 75

Gly Ser Pro Ile Asp Asp Asp Gly His Gly Thr His Thr Ala Ser Thr
1 5 10 15

Ala Ala Gly Ala Phe Val Asn Gly Ala Asn
20 25

<210> 76
<211> 26

<212> PRT
<213> *Alnus glutinosa*

<400> 76

Asn Ser Ala Arg Asp Thr Leu Gly His Gly Thr His Thr Ala Ser Thr
1 5 10 15

Ala Ala Gly Asn Tyr Val Asn Gly Ala Ser
 20 25

<210> 77
<211> 26
<212> PRT
<213> *Arabidopsis thaliana*

<400> 77

Ile Ser Ala Arg Asp Ser Thr Gly His Gly Thr His Thr Ala Ser Thr
1 5 10 15

Val Gly Gly Ser Ser Val Ser Met Ala Asn
 20 25

<210> 78
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence found in a various bacteria species

<400> 78

Asn Pro Phe Gln Asp Asn Asn Ser His Gly Thr His Val Ala Gly Thr
1 5 10 15

Val Ala Ala Leu Asn Asn Ser Ile Gly Val
 20 25

<210> 79
<211> 26
<212> PRT
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<220>
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<220>
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<222> (1)..(26)
<223> Xaa can be any amino acid

<400> 79

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa His Gly Thr His Xaa Ala Xaa Thr
1 5 10 15

Xaa Ala Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa
20 25

<210> 80
<211> 15
<212> PRT
<213> Homo sapiens

<400> 80

Gly Leu Gly Ser Ile Phe Val Trp Ala Ser Gly Asn Gly Gly Arg
1 5 10 15

<210> 81
<211> 15
<212> PRT
<213> Homo sapiens

<400> 81

Gly Lys Gly Ser Ile Phe Val Trp Ala Ser Gly Asn Gly Gly Arg
1 5 10 15

<210> 82
<211> 15
<212> PRT
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<220>
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<400> 82

Ser Lys Gly Ala Ile Tyr Val Phe Ala Ser Gly Asn Gly Gly Thr
1 5 10 15

<210> 83
<211> 15
<212> PRT
<213> Cucumis melo

<400> 83

Glu Arg Gly Ile Leu Thr Ser Asn Ser Ala Gly Asn Gly Gly Pro
 1 5 10 15

<210> 84
 <211> 15
 <212> PRT
 <213> Lycopersicon esculentum

<400> 84

Glu Arg Gly Ile Leu Val Ser Cys Ser Ala Gly Asn Asn Gly Pro
 1 5 10 15

<210> 85
 <211> 15
 <212> PRT
 <213> Alnus glutinosa

<400> 85

Glu Lys Gly Val Val Val Ser Thr Ser Ala Gly Asn Ala Gly Pro
 1 5 10 15

<210> 86
 <211> 15
 <212> PRT
 <213> Arabidopsis thaliana

<400> 86

Glu Arg Gly Ile Ser Val Ile Cys Ala Ala Gly Asn Asn Gly Pro
 1 5 10 15

<210> 87
 <211> 15
 <212> PRT
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<220>
 <223> Artificial Sequence found in various bacteria species

<400> 87

Ala Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr
 1 5 10 15

<210> 88
 <211> 15
 <212> PRT
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<220>

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<222> (1)..(15)

<223> Xaa can be any amino acid

<400> 88

Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Ala Ala Gly Asn Xaa Gly Xaa
1 5 10 15

<210> 89

<211> 21

<212> PRT

<213> Homo sapiens

<400> 89

Ser His Thr Gly Thr Ser Ala Ser Ala Pro Leu Ala Ala Gly Ile Ile
1 5 10 15

Ala Leu Thr Leu Glu
20

<210> 90

<211> 21

<212> PRT

<213> Homo sapiens

<400> 90

Thr His Thr Gly Thr Ser Ala Ser Ala Pro Leu Ala Ala Gly Ile Phe
1 5 10 15

Ala Leu Ala Leu Glu
20

<210> 91

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Artifical Sequence found in various yeast species

<400> 91

Ser His Gly Gly Thr Ser Ala Ala Ala Pro Leu Ala Ala Gly Val Tyr
1 5 10 15

Thr Leu Leu Leu Glu
20

<210> 92
<211> 21
<212> PRT
<213> *Lycopersicon esculentum*

<400> 92

Ile Ile Ser Gly Thr Ser Met Ser Cys Pro His Leu Ser Gly Val Arg
1 5 10 15

Ala Leu Leu Lys Ser
20

<210> 93
<211> 21
<212> PRT
<213> *Arabidopsis thaliana*

<400> 93

Val Met Ser Gly Thr Ser Met Ser Cys Pro His Val Ser Gly Ile Thr
1 5 10 15

Ala Leu Ile Arg Ser
20

<210> 94
<211> 21
<212> PRT
<213> *Alnus glutinosa*

<400> 94

Met Val Ser Gly Thr Ser Met Ala Cys Pro His Ala Ser Gly Val Ala
1 5 10 15

Ala Leu Leu Lys Ala
20

<210> 95
<211> 21

<212> PRT
<213> Cucumis melo

<400> 95

Ile Ile Ser Gly Thr Ser Met Ser Cys Pro His Ile Thr Gly Ile Ala
1 5 10 15

Thr Tyr Val Lys Thr
20

<210> 96
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Sequence found in various bacteria species

<400> 96

Ala Tyr Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala
1 5 10 15

Ala Leu Ile Leu Ser
20

<210> 97
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1)..(18)
<223> Xaa can be any amino acid

<400> 97

Xaa Xaa Xaa Gly Thr Ser Met Ser Xaa Pro His Xaa Xaa Gly Xaa Xaa
1 5 10 15

Ala Leu